

GenCore version 5.1.1.6
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OM protein - protein search, 'using sw model

Run on: January 4, 2006, 18:42:07 ; Search time 13 Seconds
(without alignments)
19.585 Million cell updates/sec

Title: US-10-634-895-3
Perfect score: 172
Sequence: 1 PHVGMGLETRTETWNSSSEGAWCHVRIETW 30

Scoring table: BLOSUM62
Gapop 10.0 : Gapext 0.5

Searched: 61072 seqs. 8486849 residues

Total number of hits satisfying chosen parameters: 61072

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	48	27.9	192	6	US-10-981-873-43	Sequence 43, Appl
2	47.5	27.6	3674	7	US-11-000-463-454	Sequence 454, App
3	46	26.7	334	6	US-10-793-626-282	Sequence 282, App
4	45.5	26.5	750	7	US-11-132-285-2	Sequence 2, Appli
5	45.5	26.5	1001	7	US-11-132-285-40	Sequence 40, Appl
6	45.5	26.5	1013	6	US-10-131-826A-38	Sequence 38, Appl
7	44.5	25.9	662	7	US-11-090-439-9	Sequence 9, Appli
8	44	25.6	407	7	US-11-127-877-56	Sequence 56, Appl
9	44	25.6	573	6	US-10-525-710-36	Sequence 36, Appl
10	43.5	25.3	218	6	US-10-793-626-562	Sequence 562, App
11	43.5	25.3	792	7	US-11-108-172-1127	Sequence 1127, Ap
12	43	25.0	192	7	US-11-055-822-206	Sequence 206, App
13	43	25.0	192	7	US-11-055-822-250	Sequence 250, App
14	43	25.0	200	7	US-11-055-822-204	Sequence 204, App
15	43	25.0	200	7	US-11-055-822-248	Sequence 248, App
16	43	25.0	275	7	US-11-107-028-23	Sequence 23, Appl
17	43	25.0	437	6	US-10-858-730-214	Sequence 214, App
18	43	25.0	437	6	US-10-858-730-283	Sequence 283, App
19	43	25.0	437	6	US-10-858-730-288	Sequence 288, App
20	43	25.0	480	6	US-10-510-386-12	Sequence 12, Appl
21	43	25.0	841	7	US-11-052-554A-102	Sequence 102, App
22	43	25.0	873	6	US-10-793-626-3036	Sequence 3036, Ap
23	43	25.0	1070	7	US-11-000-463-721	Sequence 721, App
24	43	25.0	1194	7	US-11-000-463-249	Sequence 249, App
25	42	24.4	684	6	US-10-714-781A-55	Sequence 55, Appl

26	42	24.4	684	6	US-10-714-781A-57	Sequence 57, Appl
27	42	24.4	684	6	US-10-714-781A-61	Sequence 61, Appl
28	42	24.4	686	6	US-10-714-781A-59	Sequence 59, Appl
29	42	24.4	705	7	US-11-102-240-162	Sequence 162, App
30	42	24.4	782	6	US-10-995-561-861	Sequence 861, App
31	42	24.4	820	6	US-10-467-657-4910	Sequence 4910, Ap
32	42	24.4	847	6	US-10-995-561-863	Sequence 863, App
33	42	24.4	847	6	US-10-995-561-865	Sequence 865, App
34	42	24.4	2647	6	US-10-821-234-1303	Sequence 1303, Ap
35	42	24.4	3433	6	US-10-714-781A-67	Sequence 67, Appl
36	41.5	24.1	253	7	US-11-054-515-1526	Sequence 1526, Ap
37	41.5	24.1	322	6	US-10-821-234-1354	Sequence 1354, Ap
38	41.5	24.1	322	6	US-10-878-556A-59	Sequence 59, Appl
39	41	23.8	600	6	US-10-606-302-3	Sequence 3, Appl
40	41	23.8	1179	7	US-11-097-125-1	Sequence 1, Appl
41	41	23.8	1196	6	US-10-995-561-921	Sequence 921, App
42	40.5	23.5	193	6	US-10-467-657-2464	Sequence 2464, Ap
43	40.5	23.5	419	6	US-10-793-626-2516	Sequence 2516, Ap
44	40.5	23.5	437	7	US-11-073-626-3	Sequence 3, Appl
45	40	23.3	107	6	US-10-467-657-6214	Sequence 6214, Ap

ALIGNMENTS

```

RESULT 1
US-10-981-873-43
; Sequence 43, Application US/10981873
; Publication No. US20050250680A1
; GENERAL INFORMATION:
; APPLICANT: Walensky, Loren D.
; APPLICANT: Korsmeyer, Stanley J.
; APPLICANT: Verdine, Gregory
; TITLE OF INVENTION: STABILIZED ALPHA HELICAL PEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00530-124001
; CURRENT APPLICATION NUMBER: US/10/981,873
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: US 60/517,848
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: US 60/591,548
; PRIOR FILING DATE: 2004-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; US-10-981-873-43

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Query Match      27.9%; Score 48; DB 6; Length 192;
Best Local Similarity 53.3%; Pred. No. 3.5;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      7 LEETRTEWTMSSEGAW 21
      |||||  - : | | |
Db      129 LETRLADWTHSSGGW 143

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RESULT 2

US-11-000-463-454

; Sequence 454, Application US/11000463

; Publication No. US20050266423A1

; GENERAL INFORMATION:

; APPLICANT: Tang, Y Tom

; APPLICANT: Liu, Chenghua

; APPLICANT: Asundi, Vinod

; APPLICANT: Chen, Rui-hong

; APPLICANT: Qian, Xiaohong B.

; APPLICANT: Wang, Zhiwei

; APPLICANT: Wehrman, Tom

; APPLICANT: Zhang, Jie

; APPLICANT: Zhou, Ping

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	172	100.0	30	3	US-09-881-710-3	Sequence 3, Appli	
2	172	100.0	30	3	US-09-881-710-11	Sequence 11, Appl	
3	172	100.0	30	4	US-10-634-895-3	Sequence 3, Appli	
4	172	100.0	30	4	US-10-634-895-11	Sequence 11, Appl	
5	172	100.0	40	5	US-10-608-147-31	Sequence 31, Appl	
6	172	100.0	48	4	US-10-311-213-32	Sequence 32, Appl	
7	172	100.0	48	5	US-10-608-029-35	Sequence 35, Appl	
8	172	100.0	685	5	US-10-500-796A-43	Sequence 43, Appl	
9	172	100.0	685	5	US-10-500-796A-45	Sequence 45, Appl	
10	172	100.0	685	5	US-10-500-796A-47	Sequence 47, Appl	
11	168	97.7	40	3	US-09-881-710-29	Sequence 29, Appl	
12	168	97.7	40	4	US-10-634-895-29	Sequence 29, Appl	
13	168	97.7	167	4	US-10-375-932-122	Sequence 122, App	
14	168	97.7	171	4	US-10-375-932-118	Sequence 118, App	
15	168	97.7	171	4	US-10-375-932-121	Sequence 121, App	
16	168	97.7	675	4	US-10-375-932-143	Sequence 143, App	
17	168	97.7	677	4	US-10-375-932-238	Sequence 238, App	
18	168	97.7	681	4	US-10-375-932-142	Sequence 142, App	
19	168	97.7	681	4	US-10-375-932-228	Sequence 228, App	
20	168	97.7	1127	4	US-10-247-960-3	Sequence 3, Appli	
21	168	97.7	3388	5	US-10-719-547-17	Sequence 17, Appl	
22	168	97.7	3391	5	US-10-719-547-21	Sequence 21, Appl	
23	168	97.7	3391	5	US-10-871-775-31	Sequence 31, Appl	
24	163	94.8	678	4	US-10-375-932-248	Sequence 248, App	
25	162	94.2	661	5	US-10-701-122-51	Sequence 51, Appl	
26	160	93.0	40	4	US-10-311-213-3	Sequence 3, Appli	
27	160	93.0	677	4	US-10-375-932-345	Sequence 345, App	

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:38:36 ; Search time 47 Seconds
(without alignments)
52.772 Million cell updates/sec

Title: US-10-634-895-3
Perfect score: 172
Sequence: 1 PHVGMGLETRTETWMSSEGAWKHVQRIETW 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	30	2	US-09-881-710-3
2	172	100.0	30	2	US-09-881-710-11
3	168	97.7	40	2	US-09-881-710-29
4	168	97.7	635	2	US-09-341-833A-7
5	168	97.7	677	2	US-09-341-833A-8
6	168	97.7	1127	2	US-08-937-195-3
7	168	97.7	1127	2	US-08-915-152-3
8	168	97.7	1127	2	US-09-376-463-3
9	168	97.7	1127	4	PCT-US96-07627-3
10	162	94.2	661	2	US-09-452-638-51
11	162	94.2	661	2	US-09-121-587A-2
12	156	90.7	39	2	US-09-881-710-12
13	156	90.7	40	2	US-09-881-710-28
14	156	90.7	76	2	US-09-881-710-1
15	152	88.4	635	2	US-09-341-833A-9
16	140	81.4	39	2	US-09-881-710-30
17	116	67.4	22	2	US-09-341-833A-5
18	107	62.2	20	2	US-09-881-710-15
19	102	59.3	20	2	US-09-881-710-17
20	85	49.4	20	2	US-09-881-710-16
21	53	30.8	140	2	US-09-270-767-47302
22	53	30.8	285	2	US-09-252-991A-25160
23	52.5	30.5	303	2	US-09-372-934-2
24	52.5	30.5	303	2	US-09-766-916-2
25	52.5	30.5	303	2	US-09-766-898-2
26	52.5	30.5	303	2	US-09-637-040C-2
27	52.5	30.5	303	2	US-10-306-249-2

28	52	30.2	104	2	US-08-996-138-24	Sequence 24, Appl
29	52	30.2	104	2	US-09-556-172-24	Sequence 24, Appl
30	52	30.2	207	2	US-08-996-138-23	Sequence 23, Appl
31	52	30.2	207	2	US-09-556-172-23	Sequence 23, Appl
32	52	30.2	309	2	US-08-996-138-22	Sequence 22, Appl
33	52	30.2	309	2	US-09-556-172-22	Sequence 22, Appl
34	52	30.2	521	2	US-08-996-138-20	Sequence 20, Appl
35	52	30.2	521	2	US-09-556-172-20	Sequence 20, Appl
36	52	30.2	541	1	US-08-604-133-2	Sequence 2, Appl
37	52	30.2	541	2	US-09-110-118-2	Sequence 2, Appl
38	52	30.2	541	2	US-09-173-151A-28	Sequence 28, Appl
39	52	30.2	541	2	US-09-578-178-2	Sequence 2, Appl
40	52	30.2	541	2	US-09-577-806-2	Sequence 2, Appl
41	52	30.2	541	2	US-09-621-502-4	Sequence 4, Appl
42	52	30.2	541	2	US-09-949-002-360	Sequence 360, App
43	52	30.2	546	2	US-09-949-002-489	Sequence 489, App
44	50.5	29.4	233	2	US-09-902-540-14590	Sequence 14590, A
45	50	29.1	283	2	US-09-252-991A-22696	Sequence 22696, A

ALIGNMENTS

RESULT 1
US-09-881-710-3
; Sequence 3, Application US/09881710
; Patent No. 6673895
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Phillipe
; APPLICANT: COURAGEOT, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671USO
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Dengue virus
US-09-881-710-3

Query Match 100.0%; Score 172; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No: 1.4e-19;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 PHVGMGLETRTETWMSSEGAWKHVQRIETW 30
Db 1 PHVGMGLETRTETWMSSEGAWKHVQRIETW 30

RESULT 2
US-09-881-710-11
; Sequence 11, Application US/09881710
; Patent No. 6673895
; GENERAL INFORMATION:
; APPLICANT: DESPRES, Phillipe
; APPLICANT: COURAGEOT, Marie-Pierre
; APPLICANT: DEUBEL, Vincent
; APPLICANT: CATTEAU, Adeline
; TITLE OF INVENTION: PRO-APOPTOTIC FRAGMENTS OF THE DENGUE VIRUS ENVELOPE GLYCOPROTEIN
; FILE REFERENCE: 209671USO
; CURRENT APPLICATION NUMBER: US/09/881,710
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/212,129
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:33:21 ; Search time 227 Seconds
(without alignments)
93.242 Million cell updates/sec

Title: US-10-634-895-3
Perfect score: 172
Sequence: 1 PHVGMGLETRTETWMSSEGAWKHVQRIETW 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	280	2	Q8QZ64 dengue viru
2	172	100.0	280	2	Q8QZ65 dengue viru
3	172	100.0	280	2	Q8QZ66 dengue viru
4	172	100.0	280	2	Q8QZ67 dengue viru
5	172	100.0	661	2	Q5VI87 dengue viru
6	172	100.0	661	2	Q5VI88 dengue viru
7	172	100.0	661	2	Q5VI89 dengue viru
8	172	100.0	661	2	Q5VI90 dengue viru
9	172	100.0	661	2	Q5VI91 dengue viru
10	172	100.0	716	2	Q6DUD2 dengue viru
11	172	100.0	757	2	Q5S8P1 dengue viru
12	172	100.0	757	2	Q5S8P2 dengue viru
13	172	100.0	757	2	Q6DUD9 dengue viru
14	172	100.0	763	2	Q5ICU8 dengue viru
15	172	100.0	775	2	Q66398 dengue viru
16	172	100.0	775	2	Q8QY07 dengue viru
17	172	100.0	3391	1	POLG_DEN26
18	172	100.0	3391	1	POLG_DEN27
19	172	100.0	3391	1	POLG_DEN2J
20	172	100.0	3391	2	O09234 DEN26
21	172	100.0	3391	2	O11875 dengue viru
22	172	100.0	3391	2	Q58Y67 dengue viru
23	172	100.0	3391	2	Q58Y69 dengue viru
24	172	100.0	3391	2	Q58Y71 dengue viru
25	172	100.0	3391	2	Q8QR27 dengue viru
26	172	100.0	3391	2	Q91U94 dengue viru
27	172	100.0	3391	2	Q68Y26 dengue viru
28	172	100.0	3391	2	Q9E7P0 dengue viru
29	168	97.7	120	2	Q67424 dengue viru
30	168	97.7	166	2	Q66346 dengue viru
31	168	97.7	661	2	Q5QIB6 dengue viru

32	168	97.7	661	2	Q5VI92_9FLAV	Q5VI92 dengue viru
33	168	97.7	661	2	Q5VI93_9FLAV	Q5VI93 dengue viru
34	168	97.7	661	2	Q5VI94_9FLAV	Q5VI94 dengue viru
35	168	97.7	661	2	Q5VI95_9FLAV	Q5VI95 dengue viru
36	168	97.7	661	2	Q5VI96_9FLAV	Q5VI96 dengue viru
37	168	97.7	745	2	Q6KEK9_9FLAV	Q6KEK9 dengue viru
38	168	97.7	775	2	Q8JYK8_9FLAV	Q8JYK8 dengue viru
39	168	97.7	775	2	Q8QY62_9FLAV	Q8QY62 dengue viru
40	168	97.7	775	2	Q8QY63_9FLAV	Q8QY63 dengue viru
41	168	97.7	779	2	Q88636_9FLAV	Q88636 dengue viru
42	168	97.7	1127	2	P89531_9FLAV	P89531 dengue viru
43	168	97.7	1127	2	P89532_9FLAV	P89532 dengue viru
44	168	97.7	1127	2	Q66454_9FLAV	Q66454 dengue viru
45	168	97.7	1127	2	Q66455_9FLAV	Q66455 dengue viru

ALIGNMENTS

RESULT 1
Q8QZ64_9FLAV
ID Q8QZ64_9FLAV PRELIMINARY; PRT; 280 AA.
AC Q8QZ64;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus; Dengue virus group.
OX NCBI_TaxID=11060;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21571640; PubMed=11714970;
RA Uzcategui N.Y., Camacho D., Comach G., Cuello de Uzcategui R.,
RA Holmes E.C., Gould E.A.;
RT "Molecular epidemiology of dengue type 2 virus in Venezuela: evidence for in situ virus evolution and recombination.";
RL J. Gen. Virol. 82:2945-2953 (2001).
DR EMBL; AF360863; AAL76291.1; -; Genomic_RNA.
DR SMR; Q8QZ64; 21-100.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0019058; P:viral infectious cycle; IEA.
DR InterPro; IPR001122; Flavi_capsidC.
DR InterPro; IPR000069; Flavi_M.
DR InterPro; IPR002535; Flavi_propep.
DR Pfam; PF01003; Flavi_capsid; 1.
DR Pfam; PF01004; Flavi_M; 1.
DR Pfam; PF01570; Flavi_propep; 1.
KW Polyprotein.
FT NON TER 280
SQ SEQUENCE 280 AA; 31846.MW; E889FDD11929CBA7 CRC64;
Query Match 100.0%; Score 172; DB 2; Length 280;
Best Local Similarity 100.0%; Pred. No. 2.6e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PHVGMGLETRTETWMSSEGAWKHVQRIETW 30
Db 211 PHVGMGLETRTETWMSSEGAWKHVQRIETW 240

RESULT 2
Q8QZ65_9FLAV
ID Q8QZ65_9FLAV PRELIMINARY; PRT; 280 AA.
AC Q8QZ65;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Polyprotein (Fragment).
OS Dengue virus type 2.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

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OM protein - protein search, using sw model

Run on: January 4, 2006, 18:34:31 ; Search time 37 Seconds
(without alignments)
78.014 Million cell updates/sec

Title: US-10-634-895-3
Perfect score: 172
Sequence: 1 PHVGMGLETRTETWMSSEGAWKHVQRIETW 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	172	100.0	775	2	A48644	polyprotein - deng
2	172	100.0	3391	1	GNWV16	genome polyprotein
3	172	100.0	3391	1	GNWV26	genome polyprotein
4	172	100.0	3391	1	GNWVJA	genome polyprotein
5	168	97.7	166	2	S40144	premembrane protei
6	168	97.7	3388	1	GNWVDP	genome polyprotein
7	168	97.7	3391	2	JS0219	polyprotein - deng
8	162	94.2	665	2	PS0043	genome polyprotein
9	159	92.4	3396	1	A42551	genome polyprotein
10	158	91.9	166	2	S09223	membrane protein -
11	156	90.7	775	2	A47311	polyprotein(C, E,
12	156	90.7	792	2	C32401	genome polyprotein
13	156	90.7	792	2	B32401	genome polyprotein
14	156	90.7	792	2	A32401	genome polyprotein
15	156	90.7	1226	1	GNWVWP	genome polyprotein
16	154	89.5	166	2	S09224	membrane protein -
17	154	89.5	166	2	S09225	membrane protein -
18	152	88.4	773	2	A47666	structural polypro
19	152	88.4	3386	1	GNWVDF	genome polyprotein
20	145	84.3	3390	1	GNWVD3	genome polyprotein
21	139	80.8	1127	1	GNWVD2	genome polyprotein
22	68	39.5	1163	1	GNWVY8	genome polyprotein
23	68	39.5	3411	1	GNWVY	genome polyprotein
24	68	39.5	3411	1	GNWVYP	genome polyprotein
25	54.5	31.7	636	2	A87134	methylmalonyl-CoA
26	54	31.4	193	2	T08300	hypothetical prote
27	54	31.4	1127	2	G71274	hypothetical prote
28	53.5	31.1	132	2	F82663	hypothetical prote
29	53	30.8	340	2	C71266	conserved hypothet

30 51 29.7 198 2 S77277 leucyltransferase
31 51 29.7 776 2 A41704 genome polyprotein
32 51 29.7 776 2 B41704 genome polyprotein
33 51 29.7 872 2 JC7380 DNA-directed DNA p
34 50 29.1 305 2 A83340 hypothetical prote
35 50 29.1 664 2 T48258 kinesi-like prote
36 50 29.1 707 2 T02835 long chain fatty a
37 50 29.1 1212 2 B82809 exodeoxyribonuclea
38 49.5 28.8 264 2 E69897 hypothetical prote
39 49.5 28.8 351 2 E84096 hypothetical prote
40 49 28.5 833 2 G75621 arylesterase/monox
41 48.5 28.2 248 2 T14547 beta-fructofuranos
42 48.5 28.2 278 2 T48426 hypothetical prote
43 48.5 28.2 605 2 AG0123 probable antigenic
44 48.5 28.2 626 2 AE0123 probable antigenic
45 48 27.9 259 2 C82148 conserved hypothet

ALIGNMENTS

RESULT 1

A48644

polyprotein - dengue virus type 2 (strain Mexican) (fragment)

C:Species: dengue virus type 2

C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 31-Dec-2004

C:Accession: A48644

R:Ruiz, B.H.; Sanchez, I.; Ortega, G.J.; Lopez, I.; Ortiz-Ortiz, L.

submitted to GenBank, October 1992

A:Description: Nucleotide sequence and deduced amino-acid sequence of the structural pr

A:Reference number: A48644

A:Accession: A48644

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-775 <RUI>

A:Cross-references: UNIPROT:Q66398; UNIPARC:UPI000000EEB45; GB:L04561; NID:G323652; PIDN

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: polyprotein

Query Match 100.0%; Score 172; DB 2; Length 775;

Best Local Similarity 100.0%; Pred. No. 1.4e-15;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PHVGMGLETRTETWMSSEGAWKHVQRIETW 30

Db 211 PHVGMGLETRTETWMSSEGAWKHVQRIETW 240

RESULT 2

GNWV16

genome polyprotein - dengue virus type 2 (strain 16681)

N:Contains: capsid protein C; envelope protein E; membrane-associated protein M; nonstru

tural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5

C:Species: dengue virus type 2

C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 31-Dec-2004

C:Accession: A42451; A43496; A43763

R:Blök, J.; McWilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Weiller, G.; Herring, B.L.; Hem

Virolgy 187, 573-590, 1992

A:Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence

A:Reference number: A42451; MUID:92188532; PMID:1312269

A:Accession: A42451

A:Molecule type: genomic RNA

A:Residues: 1-3391 <BLO>

A:Cross-references: UNIPROT:P29990; UNIPARC:UPI0000131DF5; GB:M84727; GB:M85259; NID:G3

C:Superfamily: hepatitis C virus genome polyprotein

C:Keywords: Arp; capsid protein; envelope protein; glycoprotein; nonstructural protein;

F:1-114/Product: capsid protein C #status predicted <CPC>

F:115-280/Product: membrane-associated protein M precursor #status predicted <MPP>

F:115-205/Domain: nonterminal signal sequence #status predicted <SIG>

F:206-280/Product: membrane-associated protein M #status predicted <TM1>

F:268-284/Domain: transmembrane #status predicted <EPE>

F:727-743/Domain: transmembrane #status predicted <TM2>

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: January 4, 2006, 18:32:23 ; Search time 186 Seconds
(without alignments)
70.868 Million cell updates/sec

Title: US-10-634-895-3
Perfect score: 172
Sequence: 1 PHVGMGLETRTETWMSSEGAWKHVQRIETW 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	100.0	48	5 AAE17433	Aae17433 (95-114)E
2	172	100.0	48	9 ADW12588	Adw12588 p(95-114)
3	172	100.0	685	6 ABP57874	Abp57874 Plasmid p
4	172	100.0	685	6 ABP57876	Abp57876 Plasmid p
5	172	100.0	685	6 ABP57875	Abp57875 Plasmid p
6	172	100.0	3391	2 AAW06591	Aaw06591 Polyprote
7	172	100.0	3391	2 AAW06590	Aaw06590 Polyprote
8	172	100.0	3391	4 AAE07987	Aae07987 Attenuate
9	172	100.0	3391	4 AAE07986	Aae07986 Wild-type
10	169	98.3	3391	2 AAR13166	Aar13166 Proteins
11	168	97.7	40	5 AAE17432	Aae17432 Dengue (D
12	168	97.7	167	8 ADN37497	Adn37497 Dengue vi
13	168	97.7	171	8 ADN37493	Adn37493 Dengue vi
14	168	97.7	171	8 ADN37496	Adn37496 Dengue vi
15	168	97.7	635	2 AAW75410	Aaw75410 Fusion pr
16	168	97.7	675	8 ADN37518	Adn37518 Dengue vi
17	168	97.7	677	2 AAW75411	Aaw75411 Fusion pr
18	168	97.7	677	8 ADN37613	Adn37613 Dengue vi
19	168	97.7	681	8 ADN37603	Adn37603 Dengue vi
20	168	97.7	681	8 ADN37517	Adn37517 Dengue vi
21	168	97.7	1127	2 AAW09409	Aaw09409 Dengue vi
22	168	97.7	1127	2 AAY05522	Aay05522 Dengue vi
23	168	97.7	1127	7 ADL98086	Adl98086 Dengue vi
24	168	97.7	1127	8 ADQ28716	Adq28716 Dengue vi

25	168	97.7	3388	6 AAE35314	Aae35314 Dengue vi
26	168	97.7	3391	8 ADG93314	Adg93314 DEN2 (Ton
27	163	94.8	678	8 ADN37623	Adn37623 Dengue vi
28	162	94.2	150	1 AAP91166	Aap91166 PUO-218 s
29	162	94.2	661	4 AAB84901	Aab84901 Dengue-2
30	160	93.0	677	8 ADN37720	Adn37720 Dengue vi
31	159	92.4	675	8 ADN37628	Adn37628 Dengue vi
32	159	92.4	675	8 ADN37616	Adn37616 Dengue vi
33	159	92.4	675	8 ADN37618	Adn37618 Dengue vi
34	159	92.4	675	8 ADN37612	Adn37612 Dengue vi
35	159	92.4	675	8 ADN37615	Adn37615 Dengue vi
36	159	92.4	675	8 ADN37626	Adn37626 Dengue vi
37	159	92.4	677	8 ADN37617	Adn37617 Dengue vi
38	159	92.4	3396	2 AAR43662	Aar43662 DEN1-S275
39	157.5	91.6	39	9 ADW12576	Adw12576 M1-40/DEN
40	157.5	91.6	39	9 ADW12582	Adw12582 M1-40/DEN
41	157.5	91.6	39	9 ADW12599	Adw12599 M1-40/DEN
42	157	91.3	774	8 ADG93320	Adg93320 DEN1 (Pue
43	157	91.3	775	8 ADG93318	Adg93318 DEN1 (Pue
44	156	90.7	39	5 AAE17440	Aae17440 Dengue vi
45	156	90.7	40	5 AAE17431	Aae17431 Dengue (D

ALIGNMENTS

RESULT 1
AAE17433
ID AAE17433 standard; protein; 48 AA.
XX
AC AAE17433;
XX
DT 18-APR-2002 (first entry)
XX
DE (95-114)EGFP(206-245)DEN-2 fusion protein.
XX
KW Dengue virus; PRM glycoprotein; E glycoprotein; apoptosis; virucide;
KW cancer; flavivirus infection; cytostatic; EGFP; DEN-2 protein;
KW enhanced green fluorescent protein; fusion protein; M ectodomain.
XX
OS Dengue virus; 2.
OS Dengue virus; 1.
OS Unidentified.
OS Chimeric.
XX
FH Key
FT Misc-difference 13.44
FT /note= "Encoded by GTTATC"
XX
PN WO200196376-A2.
XX
PD 20-DEC-2001.
XX
PF 18-JUN-2001; 2001WO-IB001570.
XX
PR 16-JUN-2000; 2000US-0212129P.
XX
PA (INSP) INST PASTEUR.
XX
PI Despres P, Courageot M, Deubel V, Cateau A;
XX
DR WPI; 2002-139706/18.
DR N-PSDB; AAD27335.
XX
PT Novel apoptosis inducing polypeptide fragments of Dengue virus-1 or 2 M
PT protein, useful for inducing apoptosis in a cell of a human patient
PT suffering from cancer or flavivirus infection.
XX
PS Claim 42; Fig 11; 45pp; English.
XX
CC The invention relates to pro-apoptotic fragments of the Dengue virus
CC (DEN) PRM and E glycoproteins, methods for screening molecules capable of
CC inducing apoptosis and methods of inducing apoptosis in a cell. The